We claim:

1. A method for modulating programmed cell death in a eukaryotic cell, said method comprising using (i) a nucleotide sequence of a poly(ADP-ribose) polymerase (PARP) gene of the ZAP class and (ii) a nucleotide sequence of a PARP gene of the NAP class, so as to reduce the functional level of the total PARP activity in said eukaryotic cell.

2. The method of claim 1, further comprising reducing expression of PARP genes endogenous to said eukaryotic cell by using said nucleotide sequence of said PARP gene of the ZAP class and the nucleotide sequence of said PARP gene of the NAP class.

3. The method of claim 1, further comprising reducing apparent activity of proteins encoded by the endogenous PARP genes by using said nucleotide sequence of said PARP gene of the ZAP class and said nucleotide sequence of said PARP gene of the NAP class.

4. The method of claim 1, further comprising altering the nucleotide sequence of the endogenous PARP genes with said nucleotide sequence of said PARP gene of the ZAP class and said nucleotide sequence of said PARP gene of the NAP class.

5. A method for modulating programmed cell death (PCD) in a eukaryotic cell, comprising

(A) introducing a first and a second PCD modulating chimeric gene in said eukaryotic cell, wherein said first PCD modulating chimeric gene comprises the following operably linked DNA regions:

a) a first promoter, operative in said eukaryotic cell;

b) a first DNA region, which when transcribed yields a RNA molecule, said RNA molecule being either

i) capable of reducing the functional level of a Zn-finger containing PARP protein of the ZAP class; or

ii) capable of being translated into a peptide or protein which when expressed reduces the functional level of a PARP protein of ZAP class.

c) a DNA region involved in transcription termination and polyadenylation

and wherein said second PCD modulating chimeric gene comprises the following operably linked DNA regions:

a) a second promoter, operative in said eukaryotic cell;

b) a second DNA region, which when transcribed yields a RNA molecule, said RNA molecule being either

i) capable of reducing the functional level of a PARP protein of the NAP class; or

ii) capable of being translated into a peptide or protein which when expressed reduces the functional level of a PARP protein of the NAP class

c) a DNA region involved in transcription termination and polyadenylation;

(B) reducing the total apparent PARP activity in said eukaryotic cell.

6. The method of claim 5, wherein said first transcribed DNA region encodes a sense RNA molecule, said DNA region comprising a nucleotide sequence of at least about 100 nucleotides with 75% identity to a sense DNA strand of an endogenous PARP gene of the ZAP class, and wherein said sense RNA molecule is capable of reducing the expression of said endogenous PARP gene of the ZAP class.

7. The method of claim 5, wherein said second transcribed DNA region encodes a sense RNA molecule, said DNA region comprising a nucleotide sequence of at least about 100 nucleotides with 75% identity to a sense DNA strand of an endogenous PARP gene of the NAP class, and wherein said sense RNA molecule is capable of reducing the expression of said endogenous PARP gene of the NAP class.

8. The method of claim 7, wherein said first transcribed DNA region encodes a sense RNA molecule, said DNA region comprising a nucleotide sequence of at least about 100 nucleotides with 75% identity to a sense DNA strand of an endogenous PARP gene of the ZAP class, and wherein said sense RNA molecule is capable of

reducing the expression of said endogenous PARP gene of the ZAP class.

9. The method of claim 5, wherein said first transcribed DNA region encodes an antisense RNA molecule, said DNA region comprising a nucleotide sequence of at least about 100 nucleotides with 75% identity to a complement of the DNA strand of an endogenous PARP gene of the ZAP class, and wherein said antisense RNA molecule is capable of reducing the expression of said endogenous PARP gene of the ZAP class.

10. The method of claim 5, wherein said second transcribed DNA region encodes an antisense RNA molecule, said DNA region comprising a nucleotide sequence of at least about 100 nucleotides with 75% identity to a complement of the sense DNA strand of an endogenous PARP gene of the NAP class, and wherein said antisense RNA molecule is capable of reducing the expression of said endogenous PARP gene of the NAP class.

11. The method of claim 10, wherein said first transcribed DNA region encodes an antisense RNA molecule, said DNA region comprising a nucleotide sequence of at least about 100 nucleotides with 75% identity to a complement of the sense DNA strand of an endogenous PARP gene of the ZAP class, and wherein said antisense RNA molecule is capable of reducing the expression of said endogenous PARP gene of the ZAP class.

12. The method of claim 5, wherein said first transcribed DNA region encodes a RNA molecule comprising a sense nucleotide sequence of at least about 100 nucleotides with 75% identity to the mRNA resulting from transcription of an endogenous PARP gene of the ZAP class, said RNA molecule further comprising an antisense nucleotide sequence of at least about 100 nucleotides with 75% identity to a complement of said mRNA resulting from transcription of said endogenous PARP gene of the ZAP class, wherein said sense and antisense nucleotide sequence are capable of forming a double stranded RNA region, and wherein said RNA molecule is capable of reducing the expression of said endogenous PARP gene of the ZAP class.

13. The method of claim 5, wherein said second transcribed DNA region

encodes a RNA molecule comprising a sense nucleotide sequence of at least about 100 nucleotides with 75% identity to the mRNA resulting from transcription of an endogenous PARP gene of the NAP class, said RNA molecule further comprising an antisense nucleotide sequence of at least about 100 nucleotides with 75% identity to a complement of said mRNA resulting from transcription of said endogenous PARP gene of the NAP class, wherein said sense and antisense nucleotide sequence are capable of forming a double stranded RNA region, and wherein said RNA molecule is capable of reducing the expression of said endogenous PARP gene of the NAP class.

14. The method of claim 10, wherein said first transcribed DNA region encodes a RNA molecule comprising a sense nucleotide sequence of at least about 100 nucleotides with 75% identity to the mRNA resulting from transcription of an endogenous PARP gene of the ZAP class, said RNA molecule further comprising an antisense nucleotide sequence of at least about 100 nucleotides with 75% identity to a complement of said mRNA resulting from transcription of said endogenous PARP gene of the ZAP class, wherein said sense and antisense nucleotide sequence are capable of forming a double stranded RNA region, and wherein said RNA molecule is capable of reducing the expression of said endogenous PARP gene of the ZAP class.

15. The method of claim 5, wherein said first transcribed DNA region encodes a dominant negative PARP mutant capable of reducing the apparent activity of the PARP protein encoded by an endogenous PARP gene of the ZAP class.

16. The method of claim 5, wherein said second transcribed DNA region encodes a dominant negative PARP mutant capable of reducing the apparent activity of the PARP protein encoded by an endogenous PARP gene of the NAP class.

17. The method of claim 16, wherein said first transcribed DNA region encodes a dominant negative PARP mutant capable of reducing the apparent activity of the PARP protein encoded by an endogenous PARP gene of the ZAP class.

18. The method of claim 16, wherein said dominant negative PARP mutant comprises an amino acid sequence selected from the amino acid sequence of SEQ ID

No 4 from amino acid 1 to 159 or the amino acid sequence of SEQ ID No 6 from amino acid 1 to 138.

19. The method of claim 17, wherein said dominant negative PARP mutant comprises the amino acid sequence of SEQ ID No 2 from amino acid 1 to 370, the amino acid sequence of SEQ ID No 11 from amino acid 1 to 98, or the amino acid sequence of SEQ ID No 2 from amino acid 1 to 370, wherein the amino acid sequence from amino acid 1 to 88 is replaced by the amino acid sequence of SEQ ID No 11.

20. The method of claim 5, wherein said first or said second promoter is a tissue specific or inducible promoter.

21. The method of claim 20, wherein said first or said second promoter is a fungus-responsive promoter, a nematode-responsive promoter, an anther-selective promoter, a stigma-selective promoter, or a dehiscence-zone selective promoter.

22. The method of claim 5, comprising reducing said total apparent PARP activity from about 75% to about 90% of the normal apparent PARP activity in said eukaryotic cell and protecting said eukaryotic cell against programmed cell death.

23. The method of claim 5, comprising reducing said total apparent PARP activity from about 90% to about 100% of the normal apparent PARP activity in said eukaryotic cell, and killing said eukaryotic cell by programmed cell death.

24. The method of claim 22, wherein said eukaryotic cell is a plant cell.

25. The method of claim 23, wherein said eukaryotic cell is a plant cell.

26. A method for modulating programmed cell death (PCD) in a plant cell, comprising introducing a PCD modulating chimeric gene in said plant cell, wherein said PCD modulating chimeric gene comprises the following operably linked DNA regions:

a) a plant-expressible promoter;
b) DNA region, which when transcribed yields a RNA molecule, said RNA molecule being either

i) capable of reducing the expression of endogenous PARP genes; or

ii) capable of being translated into a peptide or protein which when expressed reduces the apparent PARP activity in said plant cell.

c) a DNA region involved in transcription termination and polyadenylation

wherein the total apparent PARP activity in said plant cell is reduced from about 75% to about 100% of the normal apparent PARP activity in said plant cell.

27. A first and second chimeric PCD modulating gene as claimed in claims 5 or 21.

28. A eucaryotic cell comprising a first and second chimeric PCD modulating gene of claim 27.

29. The eucaryotic cell of claim 28, which is a plant cell

30. A non-human eukaryotic organism which comprises the eucaryotic cell of claim 28.

31. A plant comprising the plant cell of claim 29.

32. A seed of the plant of claim 31.

33. An isolated DNA sequence comprising the nucleotide sequence of SEQ ID No 1 from the nucleotide at position 113 to the nucleotide at position 3022.

34. An isolated DNA sequence comprising the nucleotide sequence of SEQ ID No 3 from the nucleotide at position 107 to the nucleotide at position 2068.

35. An isolated DNA sequence comprising the nucleotide sequence of SEQ ID No 10 from the nucleotide at position 61 to the nucleotide at position 3020.